13 60 13.2 8305 15 US-10-311-455-1542 Sequence 1542, Ap 14 59.6 13.1 5407 15 US-10-311-455-2064 Sequence 1542, Ap 15 59.4 13.0 20674 15 US-10-170-097-651 Sequence 651, App 16 59 12.9 188001 15 US-10-170-097-651 Sequence 651, App 17 58.2 12.8 858 14 US-10-198-846-7035 Sequence 7035, Ap 19 58.2 12.8 8842 15 US-10-198-846-7035 Sequence 7035, Ap 10 58 2 12.8 8842 15 US-10-340-446-7035 Sequence 31422, Ap 10 58 2 12.8 8842 15 US-10-340-4453-1422 Sequence 31422, Ap	58 12.7 6062 16 US-10-221-613-50 58 12.7 8197 15 US-10-240-485-68 58 12.7 8197 15 US-10-240-485-68 58 12.7 367378 15 US-10-312-841-1 57 6750 15 US-10-172-066-50	57.6 12.6 6050 15 US-10-11-452-06-90 57.6 12.6 6050 15 US-10-311-455-2102 57.6 12.6 6050 16 US-10-221-714A-518 57.6 12.6 6050 17 US-10-221-714A-518 57.6 12.6 6050 17 US-10-480-846-50	28 57.6 12.6 10279 15 US-10-311-455-1564 29 57.6 12.6 10279 15 US-10-311-455-1564 30 57.6 12.6 10279 15 US-10-240-5895-86 30 57 3 13 5 6055 15 152-1056.30	57.2 12.5 8085 16 US-10-221-714A-201 57.2 12.5 8085 16 US-10-221-714A-201 57.2 12.5 8085 17 US-10-311-507-71	33 57.2 12.5 8085 18 US-10-480-846-39 34 57 12.5 10866 15 US-10-311-455-2108 35 57 12.5 16258 16 US-10-257-166-120	57 12.5 53332 9 US-09-801-861-3 57 12.5 53332 14 US-10-224-562-3	56.8 12.5 91352 16 US-10-300-611-4 56.6 12.4 6013 16 US-10-221-613-226 56.6 12.4 6093 15 US-10-311-455-334 56.6 12.4 6095 15 US-10-311-455-334	56.6 12.4 6095 16 US-10-221-7144-32 56.6 12.4 6195 15 US-10-221-7144-32 56.6 12.4 16217 15 US-10-311-455-598 56.4 12.4 6131 15 US-10-311-455-663 56.4 12.4 6131 15 US-10-311-455-663	ALIGNMENTS	RESULT 1 US-09-941-042C-1 ; Sequence 1, Application US/09941042C ; Publication No. US20030018997A1 . GENEPAL TURDAMATEON.		TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING MOLECULAR DECOYS THAT ALTER PROTEIN TITLE OF INVENTION: THEREIN FILE REFRENCE: 5051-471W0 CURRENT APPLICATION NUMBER: US/09/941,042C CURRENT FILLING DATE: 2002-08-20 PRIOR APPLICATION NUMBER: US 60/229,198	<pre>FILON FILING DATE: 2000-08-30 FILONES OF SEQ ID NOS: 4 FILONES: PATENTIN VERSION 3.1 FILONES FILO</pre>) LENVIII 450 ; TYPE: DNA ; ORGANISM: Nicotiana tabacum US-09-941-042C-1	Query Match 100.0%; Score 456; DB 10; Length 456; Best Local Similarity 100.0%; Pred. No. 3e-68; Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	0y 1 GGAAACATATTCAATACATTGTAGTAGTAGTCGTAAATGGTGGCTT 60 0y	QY 61 GCTAATAAAGATACTTGAAATAGCTTAGTTTAAATAATAGCATAATAGGATTATGGA 10 V V V V 10 QY V V V 10
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model	Run on: November 13, 2004, 02:18:46 ; Search time 375 Seconds (without alignments) 6567.600 Million cell updates/sec	Title: US-09-941-042C-1 Perfect score: 456 Sequence: 1 ggaaacatattcaatacattggtaaaagcagttacagag 456	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 3625171 seqs, 2700493622 residues	er of hits sa seg length:	length: 2000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries			~ ~ O H O *	0 4° 0	<pre>16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:* 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:* 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:* 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:* 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:* 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*</pre>	Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	summaries Query	Score Match Length DB ID 456 100.0 456 10 US-09-941-042C-1 456 100.0 456 17 US-10-363-069-1 560uenc	3 66.6 14.6 5145 15 US-10-511-455-121 Sequent 5 66.6 14.6 5145 15 US-10-311-455-17 Sequenc 6 61 13.6 5175 15 US-10-311-455-1541 Sequenc 6 61 13.4 6175 15 US-10-311-455-1280 Sequenc	C / 61 13.4 13.6001 15 US-10-721-1/7 General G

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13574 13694 13814 ö 78 138 198 258 318 259 ATATTTTTTCAATTTATTATAAAATAAAAAACTTACCCTAATTATCGGTACAGTTAT 318 Sequence 17, Application US/10480846 Sequence 17, Application US/10480846 Publication No. US20040219549A1 GENERALI INPORMATION: APPLICANT: Distler, Jurgen APPLICANT: Model, Fabian APPLICANT: Adorjan, Peter TITLE OF INVENTION: Method and nucleic acids for the differentiation TITLE OF INVENTION: Method and nucleic acids for the differentiation TITLE OF INVENTION: Method and nucleic acids for the differentiation TITLE OF INVENTION: Method and nucleic acids for the differentiation TITLE OF INVENTION: Method and nucleic acids for the differentiation TITLE OF INVENTION NUMBER: US/10/480, 846 CURRENT FILING DATE: 2003-06-14 PRIOR APPLICATION NUMBER: PC7/EP02/06603 PRIOR APPLICATION NUMBER: P1.1128509.4 NUMBER OF SEQ ID NOS: 116 SED ID NO 17 LENCTA: 18997 AATAGCTTAGTTTAAATAAATAGCATAATAGATTTTAGGAATTAGTATTTGAGTTTA 19 TIGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCCTAATAAAGATACTTGA TATTAGTTTTTAAACTTACTATATATTTTTCATATGTAAAATTTTAATCGGTATAGTTCG ATTACTTATTGACTTGTAACAGTTTTTAATTACCAAGGCCCCATGAAAAATTTAATGCTT Gaps ; FEATURE: . OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-480-846-11 ö Length 18997 Indels Score 60.4; DB 18; Pred. No. 0.91; 0; Mismatches 156; US-10-311-455-1549 Sequence 1549, Application US/10311455 Publication No. US20030143606A1 Publication No. US20030143606A1 GENERAL INFORMATION: APPLICANT: OLEK, Alexander APPLICANT: DELEVENBROCK, Christian APPLICANT: BERLIN, Kurt Query Match 13.2%; Best Local Similarity 49.7%; Matches 154; Conservative 0 TYPE: DNA ORGANISM: Artificial Sequence 13815 GATTTGTTTT 13824 13815 GATTIGTITT 13824 319 AGATTTATAT 328 319 AGATTTATAT 328 RESULT 11 US-10-480-846-17 56 139 199 13695 13755 RESULT 12 q g _ PD 8 \mathcal{S} å 8 ß 5 8 a 8 å δ q \mathcal{S} current control c 13754 13634 13694 13515 TIGAGGITITTTTATTITTGGGGATTTTGATTIATATTTÄTIGAÄATAATTTGG 13574 13695 TATTATTAATAGTTTTTTTTTTTTTTAGATTTTTTTTAATTGAAAATGATAAG 13754 ö 138 . 0 258 198 259 ATATTTTTCAATTTATTATTATAAAAAAACTTACCCTAATTATCGGTACAGTTAT 318 199 TATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTTAATCGGTATAGTTCG 258 79 AATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATTAGTATTTTGAGTTTA 138 198 78 78 79 AATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATTAGTATTTTGAGTTTA 139 ATTACTTATTGACTTGTAACAGTTTTTTATTATTCCAAGGCCCATGAAAAATTTAATGCTT 13695 TATTATTAATAGTTTTTTTTTTTTTTTAGATTTTTTAGATTAATTGAAATGATAAG 19 TTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCTAATAAAGATACTTGA TTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCTAATAAAGATACTTGA TATTAGTTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTTAATCGGTATAGTTCG ATTACTTATTGACTTGTAACAGTTTTTTATTATTCCAAGGCCCATGAAAAATTTTAATGCTT Gaps Gaps Length 18997; ö OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) .. 0 Indels Mismatches 156; Indels Score 60.4; DB 17; Pred. No. 0.91; 0; Mismatches 156; :0 Query Match 13.2%; Best Local Similarity 49.7%; Matches 154; Conservative (ORGANISM: Artificial Sequence 13815 GATTTGTTTT 13824 Conservative 319 AGATTTATAT 328 154; RESULT 10 US-10-311-507-31 US-10-311-507-31 139 19 13575 199 13755 TYPE: DNA FEATURE: Matches പ്പ δ dd δ dC δ q δ q δ g 8 q \mathcal{S} qq δ q δ qq 8

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APPLICANT: OLEX, Alexander APPLICANT: OLEX, Alexander APPLICANT: PIEPENBROCK, Christian APPLICANT: PIEPENBROCK, Christian APPLICANT: BIBLUN, Kurt TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determi TITLE OF INVENTION: cytosine methylation TITLE OF INVENTION NUMBER: US/10/311,455 CURRENT APPLICATION NUMBER: PCY/EPO1/07537 PRIOR APPLICATION NUMBER: PC//EPO1/07537 PRIOR APPLICATION NUMBER: PC//EPO1/07537 PRIOR APPLICATION NUMBER: DE 10043826.1 PRIOR PRIOR PATE: 2000-09-01 NUMBER OF SEQ ID NOS: 2424 TERMINE OF SEQ ID NOS: 2424 ť 4437 тааааттетедааааттааттааттаассассестттаттетататааа 4496 ö 2001 2181 ö 1941 4436 247 183 187 127 123 243 248 GGTATAGTTCGATATTTTTTTTTTTTTTTTTTAAAAAAACTTACCTTAATTATC 307 67 128 TTTTGAGTTTAATTACTTATTGCTTGTAACAGTTTTTATAATTCCAAGGCCCCATGAAAA 68 AAGATACTTGAAATAGCTTAGTTTAAATAATAGCATAATAGATTTTAGGAATTAGTA 168 ATTTAATGCTTTTATAGTTTTTAAACTTACTATATAAATTTTTTCATATGTAAAATTTTAATC 124 AGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTTATAATTCCAAGGCCCCATG 8 TATTCAATACATTGTAGTTTGCTACTCCTAAATCGCTAGAATACTTTGTGCCTTGCTAATA 308 GGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAAACCTAAAAAT 363 64 AATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATT 184 AAAAATTTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTT Gaps Gaps ;; 0 ö (Homo sapiens) Length 5407; DB 15; Length 8305; 0.87; Indels 0; Mismatches 185; Indels ; OTHER INFORMATION: chemically treated genomic DNA US-10-311-455-2064 Score 59.6; DB 15; Pred. No. 0.91; 0; Mismatches 139; Score 60; Pred. No. RESULT 14 US-10-311-455-2064 Sequence 2064, Application US/10311455 Publication No. US20030143606A1 GENERAL INFORWATION: 13.2%; 48.0%; TYPE: DNA ORGANISM: Artificial Sequence Query Match 13.1%; Best Local Similarity 50.7%; Matches 143; Conservative Query Match 13.23 Best Local Similarity 48.0³ Matches 171; Conservative 5407 FEATURE: LENGTH 8 g 5 g 8 g δ PP PP q g å δ q q \mathcal{S} q 8 \mathcal{S} sequence 1542, Application US/10311455 Sequence 1542, Application US/10311455 Publication No. U52003014366A1 GENERAL INFORMATION: APPLICANT: DLEK, Alexander APPLICANT: DLEK, Alexander APPLICANT: DERLIN, Kurt APPLICANT: DERLIN, Kurt TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern TITLE OF INVENTION NUMBER: U5/10/311,455 CURRENT FILING DATE: 2002-12-16 PRIOR APPLICATION NUMBER: D01/07537 PRIOR APPLICATION NUMBER: DE 10032529.7 PRIOR APPLICATION NUMBER: DE 10032529.7 PRIOR APPLICATION NUMBER: DE 10033529.7 PRIOR PLING DATE: 2000-09-01 NUMBER OF SEQ ID NOS: 2424 LENGTH: B305 LENGTH: B305 TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern TITLE OF INVENTION: cytosine methylation TITLE OF INVENTION: cytosine methylation CURRENT FILING DATE: 5003-12-16 CURRENT FILING DATE: 2002-12-16 REIOR APPLICATION NUMBER: US/10/317 PRIOR FILING DATE: 2001-07-02 PRIOR FILING DATE: 2000-07-02 PRIOR FILING DATE: 2000-06-30 PRIOR FILING DATE: 2000-06-30 PRIOR FILING DATE: 2000-06-30 PRIOR FILING DATE: 2000-06-30 PRIOR FILING DATE: 2000-09-01 NUMBER: DATE: 2000-09-01 NUMBER OF SED ID NOS: 2424 LENGTH: 5525 2318 ô ATAAGGGATTTTTAGATATATATATTTATATTTAAATGTATGTTTTTAAGAATTA 2258 244 124 125 GIATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCATGA 184 ATCGGTATAGTTCGATATTTTTTTTTTTTTTATAAAAACTTACCTTAATT 304 185 AAAATTTAATGCTTTATTAGTTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTA ATAAAGATACTTGGAAATAGCTTAGTTTAAATATAAATAGCATAATAGGATTAGGAATTA GAATTTTGAATTTGTTTTAGTTTAGGTTTGATATTATATATAGATTTGATTTGATTTGATTTGA Gaps / FEATURE: / CTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1549 :0 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1542 Length 5925; Indels Grarrfrrgragradrrantaaraariaaraargegrrfr 2479 305 ATCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTT 345 Score 60.2; DB 15; Pred. No. 0.74; 0; Mismatches 138; TYPE: DNA ORGANISM: Artificial Sequence TYPE: DNA ORGANISM: Artificial Sequence FEATURE: Query Match 13.2%; Best Local Similarity 50.9%; Matches 143; Conservative Query Match Best Local Similarity RESULT 13 US-10-311-455-1542

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Best Local Similarity 100.0%; Pred. No. 1.4e-86;Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;0y1 GGAAACATATTCAATACATTGTAGTTTGCTACTCATAATAGTTTTGGCCCTT 600y61 GCTAATAAAGATACTTGAATAGCTTAGTTTAATAATAACGCTAGAATACTTTGGCCCTT 600y61 GCTAATAAAGATACTTGAAATAGCTTAGTTTAAATAATAAAAGATATTAGGATAC0y61 GCTAATAAAGATACTTGAAATAGCTTAGTTTAAATAATAAAAGAATATTAGGATAC0y61 GCTAATAAAGATACTTGAAATAGCTTAGTTTAAATAAAAGAATATTAGGATACTTGGGCGCT 600y121 ATTAGTATTTGAGTTTGAATAGCTTAGTTTAAATAAAAGAATATTAGGATAATAGAATATTAGGATAC0y121 ATTAGTATTTGAGTTTAATTACTTAATAGATATAAAAAGAATATTAAGGATAATAGAATAAGGAGG	<pre>3.1 ANTOGATIGATICATION CONTROL CATACAGAG 456 4.21 CCTAGTTGTTGTTATAGGTAAAAGCAGTTACAGAG 456 4.21 CCTAGTTGTTGTTATAGGTAAAAGCAGTTACAGAG 456 4.21 CCTAGTTGTTGTTATAGGTAAAAGCAGTTACAGAG 456 4.21 CCTAGTTGTTATAGGTAAAAAGCAGTTACAGAG 456 4.21 CCTAGTTGTTATAGGTAAAAAGCAGTTACAGAG 456 4.21 CCTAGTTGTTATAGGTAAAAAGCAGTTACAGAG 456 4.21 CCTAGTTGTTATAGGTAAAAAGCAGTTACAGAG 456 4.20 CATAGTTGTTATAGGTAAAAAGCAGTTACAGAG 456 4.21 CCTAGTTGTTATAGGTAAAAAGCAGTTACAGAG 456 4.21 CCTAGTTGTTATAGGTAAAAAGCAGTTACAGAG 456 4.21 CCTAGTTGTATA AAAAAAAGCAGTTACAGAG 456 4.20 CATAGTTGATTA AAAAAAGCAGTTACAGAG 456 4.20 CATAGTTGATTA AAAAAAAAAAAAAAAAAAAAAAAAAA</pre>
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/ Patent No. 5837876 TELECOMMUNICATION INFORMATION: TELEPHONE: 919-420-2200 TELEFAX: 919-881-3175 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) PCT-US96-12158-4 TELEPAX: 919-881-3175 TELEPAX: 919-882 ID NO: 4: SEQUENCE CHARACTERISTISS: LENGTH: 1294 base pairs TYPE: nucleic acid STRANDEDNESS: single 28234 US-08-508-786-3 301 241 421 685 ZIP: RESULT q a g qd P P 8 å δ q \mathcal{S} å 8 \mathcal{S} δ δ δ ; 0 120 325 GCTAATAAGGATACTTGAAATAGGCTTAAGTTTAAATATAAAATAGCATAATAGGATTTTAGGA 384 181 ATGAAAAATTTTAATGCTTTAATTAGTTTTAAACTTACTATAAATTTTTCATATGTAAAAA 240 445 ATGAAAAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAA 504 AATTATCGGTACAGTTATAGATTTATATAAAATCTACGGTTCTTCAGAAGAAACCTAAA 360 AATCGGTTCGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACT 420 AATCGGTTCGGGGGGGGGGGGGGGGTTCGGGTTTAGGTCGATTTTCCAAAAAATATTCATTGACACT 684 ATTAGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTTATAATTCCAAGGCCC 180 AATTATCGGTACAGTTATAGATTTATATATAAAATCTACGGTTCTTCAGAAGAAACCTAAA 624 60 SCTPATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGA GGAAACATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTT Gaps ö Length 1294; 0; Indels Sequence 4, Application PC/TUS9612158 GENERAL INFORMATION: APPLICANT: Conkling, Mark A. APPLICANT: Mandini APPLICANT: Song, Wan TITLE OF INVENTION: Root Cortex Specific Gene Promoter NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park & ADDRESSEE: Gibson SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US96/12158 CCTAGTTGTTGTTATAGGTAAAAAGCAGTTACAGAG 456 ccractrerrerraraceraaaaccacrracacage 720 Query Match 100.0%; Score 456; DB 2; Best Local Similarity 100.0%; Pred. No. 1.4e-86; Matches 456; Conservative 0; Mismatches 0; ATTORNEY/AGENT INFORMATION: NAME: Sibley Kenneth D. REGESTRATION NUMBER: 31,665 REGESTRATION NUMBER: 31,665 STREET: Post Office Drawer 34009 CITY: Charlotte STATE: North Carolina COUNTRY: USA ZIP: 28234 ZIP: 28234 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: TEM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS TYPE: nucleic acid TYPE: nucleic acid TYPE: single MOLECULE TYPE: DNA (genomic) US-08-508-786-4 TYPE: nucleic acid STRANDEDNESS: single FILING DATE: CLASSIFICATION: RESULT 4 PCT-US96-12158-4 121 241 301 565 625 421 361 685 265 C) qd qq q q δ q \mathcal{F} δ qq 2 qq 5 δ đ ð \mathcal{S}

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RESULT 12 PCT-US96-12158-6 FCT-US96-12158-6 Sequence 6, Application PC/TUS9612158 Generee 6, Application PC/TUS9612158 GENERAL INFORMATION: APPLICANT: CONKING, Mark A. APPLICANT: Song, Mark A. APP	CITY: CLAIOTEE STATE: North Carolina COUNTY: USA ZIF: 28234 ZIF: 28234 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPDY disk COMPUTER: IBW PC COMPALIA COMPUTER: IBW PC COMPALIA COMPUTER: PROPERTING CONTUTER: PROPERTING SOFTWARE: PRENETING RELACE #1.0, Version #1.30 OPERATION NUMBER: PCT/US96/12158 FILING DATE: APPLICATION NUMBER: PCT/US96/12158 FILING DATE: CLASSIFICATION NUMBER: PCT/US96/12158 FILING DATE: CLASSIFICATION NUMBER: PCT/US96/12158 FILING DATE: CLASSIFICATION NUMBER: PCT/US96/12158 FILING DATE: CLASSIFICATION NUMBER: 31,665 REGISTRATION NUMBER: 7000000000000000000000000000000000000	INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: INFORMATION FOR SEQ ID NO: 6: STRANDEDIES CHARACTERISTICS: TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) PCT-US96-12158-6 Query Match 32.5%; Score 148; DB 5; Length 722; Best Local Similarity 100.0%; Pred. No. 1.6e-22; Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 309 GTACAGTTATAGATTATATAAAAATCTACGGGTTCTTCAGAAGAAACCTAAAAATCGGTT 368 1<	RESULT 13 US-09-916-28 Sequence 288, Application US/08998416 Facent No. 6239264 GENERAL INFORMATION: APPLICANT: Philippsen, Peter APPLICANT: Pohlmann, Rainer APPLICANT: Steiner, Sabine APPLICANT: Wordland, Jurgen APPLICANT: Knechtle, Philipp APPLICANT: Rebischung, Corinne
Db1199TTAATGGTATAGTTGATTTTTTAAAATAAAAAAAAAAA	RESULT 11 US-08-508-786-6 Sequence 6, Application US/08508786 Patent No. 583/376 GENERAL INFORMATION: APPLICANT: Conkling, Mark A. APPLICANT: Conkling, Mark A. APPLICANT: Song, Wen TITLE OF INVENTION: Root Cortex Specific Gene Promoter MADER OF SECURNCES: 9 NUMBER OF SECURNCES: 9 NUMBER OF SECURCES: 9 NUMBER OF SECURCES: 9 NUMBER OF SECURCES: 9 NUMBER OF SECURCES: 9 NUMBER OF SECURCES: 9 NUMBER OF SECURCES: 9 NUMBER OF SECURCES: 9 NUMBER OF SECURCES: 9 NUMBER OF SECURCES: 9 NUMBER OF SECURT SOLD SIBLEY, Bell, Seltzer, Park & ADDRESSEE: Gibson STREET: Post Office Drawer 34009 CITY: Charlotte STATE: NO. 5837876th Carolina CONNTRY: USA CONNTRY: USA	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC COMPALIDE OPERATING SYSTEM: PC-DOS/NS-DOS SOFTWARE: PALENTIN RAIES #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/509,786 FILING DATE: CLASSIFICATION NUMBER: US/08/509,786 ATTORNEY/AGENT INFORMATION: NAME: SIDIEY, KENNETH D: RECISTRATION NUMBER: 31,665 REFERENCE/DOCKET NUMBER: 5051-294 TELECOMMUNICATION INFORMATION:	NB: 919-420-2200 : 919-801-3175 : 501-801-3175 : 712 base pairs nucleic acid DNESS: single Y: linear Y: linear TYPE: DNA (genomic 6	

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APELICANT: CUMMENT, 1.1.1 APELICANT: COHEN, ANDICK TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING FILE REFERENCE: GENERS INVOLVED IN ARACHIDONIC ACID METABOLISM CURRENT APPLICATION NUMBER: 05/09/641, 638 CURRENT APPLICATION NUMBER: 05/06/330 PRIOR APPLICATION NUMBER: 05/05/330 PRIOR APPLICATION NUMBER: 05/05/330 PRIOR APPLICATION NUMBER: 05/05/330 PRIOR APPLICATION NUMBER: 05/05/330 PRIOR APPLICATION NUMBER: 05/05/330 PRIOR APPLICATION NUMBER: 05/05/330 PRIOR PLING DATE: 1999-05-07 PRIOR APPLICATION NUMBER: 05/05/25/367 PRIOR APPLICATION NUMBER: 05/07/33,200 PRIOR PLING DATE: 1999-03-23 PRIOR APPLICATION NUMBER: 05/0119,917 PRIOR APPLICATION NUMBER: 05/0119,917 PRIOR APPLICATION NUMBER: 05/0119,917 PRIOR APPLICATION NUMBER: 05/0119,917 PRIOR APPLICATION NUMBER: 05/0119,917 PRIOR APPLICATION NUMBER: 05/0119,917 PRIOR APPLICATION NUMBER: 05/0119,917 PRIOR PLING DATE: 1999-03-23 PRIOR APPLICATION NUMBER: 05/0119,917 PRIOR PLING DATE: 1999-03-23 PRIOR APPLICATION NUMBER: 05/0119,917 PRIOR PLING DATE: 1999-03-23 PRIOR APPLICATION NUMBER: 05/0119,917 PRIOR PLING DATE: 1999-03-23 PRIOR PLING DATE: 1999-03-23 PRIOR APPLICATION NUMBER: 05/0119,917 PRIOR PLING DATE: 1999-03-23 PLING DATE: PLING DATE: 1999-03-23 PLING DATE: PLING DATE: 1999-03-23 PLING DATE: PLING DATE: 1999-03-23 PLING DATE: PLING DATE: 1999-03-23 PLING DATE: PLING DATE: 1999-03-23 PLING DATE: PLING DATE: 1999-NAME/KEY: misc_feature LOCATION: 1123-3123 LOCATION: 1123-3123 OTHER INFORMATION: 5'regulatory region NAMM/KEY: exon LOCATION: 3124..3297 OTHER INFORMATION: exon 1 LOCATION: 3871..4072 OTHER INFORMATION: exon 2 OTHER INFORMATION exon 14 OTHER INFORMATION exon 14 NAME/KEY: misc feature LOCATION 17555_.20674 OTHER INFORMATION: 3'regulatory region Blumenfeld, Marta Bougueleret, Lydie LOCATION: 6349..6509 OTHER INFORMATION: exon 6 NAME/KEY: exon LOCATION: 7379..7522 OTHER INFORMATION: exon NAME/KEY: exon LOCATION: 8654.8854 OTHER INFORMATION: exon 8 NAME/KEY: exon LOCATION: 13308..13429 OTHER INFORMATION: exon 11 INFORMATION: exon 12 ION: 16775..16945 INFORMATION: exon 13 INFORMATION: exon 10 Chumakov, Ilya LOCATION: 5996..6099 OTHER INFORMATION: exon 5 NAME/KEY: exon CCATION: 5758..5880 OTHER INFORMATION: exon 4 INFORMATION: exon 9 TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: exon LOCATION: 12254..12340 NAME/KEY: exon LOCATION: 12854..13023 16567..16667 .17554 NAME/KEY: exon LOCATION: 5996..6099 GENERAL INFORMATION: NAME/KEY: exon LOCATION: 16775. NAME/KEY: exon LOCATION: 1656 NAME/KEY: exon APPLICANT: APPLICANT: APPLICANT : NOI OTHER DTHER DTHER DTHER

.. H 293 64 AATAAAGATACTTGAAATAGCTTAGTTTAAATATAATAGCATAATAGATTTTAGGAATT 123 124 AGTATTTTGAGTTTAATTACTTATTG--ACTTGTAACAGTTTTTATTAATTCCAAGGCCCA 181 241 533 c 4 AACATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCT TGAAAAATTTAATGCTTTAATTTAAACTTACTATATAAAATTTTTCCATATGTAAAAT 474 TTTAACTTTAATTTCTTATTATTAATTTTAATTAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAA Gaps .. N GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII AND USES THEREOF 1152 Query Match 13.3%; Score 60.6; DB 3; Length 837; Best Local Similarity 51.1%; Pred. No. 0.00024; Matches 168; Conservative 0; Mismatches 159; Indels ADDRESSEE: No. 6239264artis Corporation STRET: 3054 Cornwallis Road GTTY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA 302 ATTATCGGTACAGTTATAGATTTATATAA 330 534 тттаттаттаттаттааттаатта RESULT 14 US-09-641-638-651 , Sequence 651, Application US/09641638 ; Patent No. 6432648 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE: TITLE OF INVENTION: GENU TITLE OF INVENTION: AND NUMBER OF SEQUENCES: 11: CORRESPONDENCE ADDRESSE: ADDRESSEE: NO. 6239264 ORGANISM: PAG1241RP US-08-998-416-288 182 8 q δ q δ qq å \mathcal{S} g δ 8

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5 : polymorphic base C or T	: polymorphic base A or	0 : polymorphic base A or G 1 : polymorphic base A or T	8 : polymorphic base A or G	: polymorphic base A	: polymorphic base A or	••	6 : deletion of CTG	4 : polymorphic base G or T	8 : polymorphic base C or T	: polymorphic base C or T	: polymorphic base C or	: polymorphic base A or	: polymorphic base A or	3 : polymorphic base C or T	<pre>/ Score 59.4; DB 4; Length 20674; / Pred. No. 0.00062; 0; Mismatches 156; Indels 0; Gaps 0;</pre>	110		GATTTTAGGAATTAATTTAGGTTTAATTACTTATTGACTTGTAACAGTTTTANAAT 170 	TCCAAGGCCCATGAAAATTTAATGCTTTAATTAGTTTAACTTACTATATAAATTTTTC 230 ************************************		AATITTAATATTAATTAATTTAATATTAATATTTAACTTAATTTAATTTAATATTA AATITTAATATTAATTAATT
<pre>i LOCATION: 6429 i OTHER INFORMATION: 10-347-165 i NAME/KEY: allele</pre>	DCCATION: 6467 OTHER INFORMATION: 10-347-203 NAME/KEY: allele LOCATION: 6484	<pre>> OTHER INFORMATION: 10-347-220 > NAME/KEY: allele > LOCATION: 6534 > OTHER INFORMATION: 10-347-271 > NAME/KEY: allele</pre>	CCATION: 6611 CTHER INFORMATION: 10-347-348 NAME/KRY: allele	RMATION: 10-348 allele 3608	OTHER INFORMATION: 10-343-4/ NAME/KEY: allele DCCATION: 865B	NAME/KEY: allele LOCATION: 8703 COTHER INFORMATION: 10-349-142	DIAL CONTRACT STATE STATE DIAL STATE DIAL DIAL STATE	DCATTON: 8785 DOTHER INFORMATION: 10-349-224 NAME/XEY: allele	<pre>bucklion: bucklion: 10-349-368 DATHER INFORMATION: 10-349-368 NAMF/KEY: allele construction: 13171</pre>	DCCALIDON: 12111 CUTHER INFORMATION: 10-350-72 NAME/KEY: allele CCCATION: 12429	N: 10-350	CTHER INFORMATION: 10-507-170 NAMEYKEY: allele . LOCATION: 13492	; OTHER INFORMATION: 10-507-321 ; NAMEZ/KRY: allele ; LOCATION: 13524	OTHER INFORMATION: 10-507-353 NAME/KEY: allele DCATION: 13535	Query Match 13.0%, Best Local Similarity 49.5%, Matches 153; Conservative	QY 51 TTTGTGCCTTGCTAATAV	11064	QY 111 GATTTTAGGAATTAGTAY Db 11124 TTAAAATTAAAATTTTAU	QY 171 TCCAAGGCCCATGAAAA	231	Db 11244 AATTTTAATATTAATATTAATATT
: polymorphic base C or T	: polymorphic base C or T	: polymorphic base C or T . deletion of C	age -	: polymorphic base C or T	: insertion of T	polymorphic base G or C	: polymorphic base A or G	base C or	: polymorphic base A or G	: polymorphic base A or G	: polymorphic base A or G	: deletion of C	: polymorphic base C or T	: polymorphic base C or T	: polymorphic base G or T	: polymorphic base A or G	: polymorphic base A or G	: polymorphic base G or C	: polymorphic base C or T	: polymorphic base A or G	: polymorphic base G or C
10-508-191	10-508-245	10-509-284	10-510-173	10-511-62	10-511-337	10-512-36	010 CT 01		10-513-352	10-513-365	, 2-206-81	10-343-231	12-206-366	10-343-278	10-343-339	10-346-23	10-346-141	10-346-263	10-346-305	10-347-74	10-347-111
NAME/KEY: allele LOCATION: 1128 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 1182 OTHER INFORMATION: NAME/KEY: allele	1559 DRMATION allele 1570	UTHER INFORMATION: NAME/KEY: allele LOCATION: 1827 OTHER INFORMATION: NAME/VEV: allelo	allele 2048 DRMATION: allele	<pre>LOCATION: 2323 COTHER INFORMATION: NAME/KEY: allele . LOCATION: 2341</pre>	ORMATION allele 2623	CUTER INFORMATION: NAME/KEY: allele	INFC EV:	NAME/KEY: allele LOCATION: 2934 OTHER INFORMATION:	; NAME/KEY: allele ; LOCATION: 2947 ; OTHER INFORMATION: ; NINNE/VEV: allele	LOCATION: 3802 OTHER INFORMATION: 1 NAME/KEY: allele	LOCATION: 4062 CTHER INFORMATION: NAME/KEY, AILEIE	LOCATION: 4088 CTHER INFORMATION: NAME/KEV. 311210		<pre>bocation: 41/0 contex information:</pre>		; OTHER INFORMATION: ; NAME/KEY: allele	NION: KEY:	9	DUCATION: 5338 OTHER INFORMATION: NAME/KEY: allele	; LOCATION: 6375 ; OTHER INFORMATION: ; NAME/KEY: allele

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LOCATION: 86458854 CTHER INFORMATION: exon 8 FEATURE: NAME/KEY: exon LOCATION: 1225412340 CTHER INFORMATION: exon 9 FEATURE: NAME/KEY: exon	LOCATION: 12854.13023 OTHER INFORMATION: EXON 10 NAME/KEY: EXON LOCATION: 13308.13429 LOCATION: 13308.13429 OTHER INFORMATION: EXON 11 RAME/KEY: EXON LOCATION: 16567.16667 OTHER INFORMATION: EXON 12 FEATURE:	NAME/KEY: exon LOCATION: 1677516945 OTHER INFORMATION: exon 13 FEATURE NAME/KEY: exon OTHER 1706317554 OTHER 1706317554 OTHER INFORMATION: exon 14 FEATURE: misc_feature LOARION: 17552.20574 OTHER INFORMATION: 3'regulatory region	FEATURE: NAME/KEY: allele COATION: 1128 COTHER INFORMATION: 10-508-191 : polymorphic base C or T FEATURE: NAME/KEY: allele LOCATION: 1182 COTHER INFORMATION: 10-508-245 : polymorphic base C or T	FEMTURE: NAME/KEY: allele LOCATION: 1559 CTHER INFORMATION: 10-509-284 : polymorphic base C or T FEATURE: NAME/KEY: allele LOCATION: 1570 CATIER INFORMATION: 10-509-295 : deletion of C PRATTER :	NAME/KEY: allele LCCATION: 1827 OTHER INFORMATION: 10-510-173 : variable motif ATTTA or TTTTT FEATURE NAME/KEY: allele LCCATION: 2048 OTHER INFORMATION: 10-511-62 : polymorphic base C or T FEATURE	NAME/KEY: allele LCOATION: 2323 COTHER INFORMATION: 10-511-337 : insertion of T FEATURE NFORMATION: 10-511-337 : insertion of T NAME/KEY: allele COTHER INFORMATION: 10-512-36 : polymorphic base G or C FEATURE NFORMATION: 10-512-36 : polymorphic base G or C NAME/KEY: allele	DCHLON: 2623 CTHER IFRORWATION: 10-512-318 : polymorphic base A or G FEATURE: NAME/KEY: allele COCATION: 2832 COTHER INFORMATION: 10-513-250 : polymorphic base A or G FEATURE: NAME/KE: allele LOCATION: 2844
QY 291 AACTTACCCTAATTATCGGTACAGTTATAGATTATAAAAATCTACGGTTCTTCAGAA 350 b 11304 ATTTAACTTAATTTAATTTAATTTAAATTAATTTTAATATTTTAATTTT	RESULT 15 US-10-10-097-651 5 Sequence 651, Application US/10170097 5 Batent No. 6794143 6 GENERAL INFORMATION: 7 APPLICANT: Buugnelerd, Matta 7 APPLICANT: Chumakov, Ilya 7 APPLICANT: Chumakov, Ilya 7 APPLICANT: Cohen, Annick 7 APPLICANT: Cohen, Annick 7 TITLE OF INVENTION: SILVED FROM GENOMIC REGIONS CARRYING	TITLE OF INVENTION: GENES INVOLVED IN ARCHIDONIC ACID METABOLISM FILE REFERENCE: GEN-T114XC2D1 CURRENT APPLICATION UNMER: US/10/170,097 CURRENT FILING DATE: 2000-06-10 PRIOR APPLICATION NUMBER: US 09/641,638 PRIOR FILING DATE: 2000-08-16 PRIOR FILING DATE: 2000-08-16 PRIOR FILING DATE: 2000-08-16 PRIOR FILING DATE: 2000-08-16 PRIOR FILING DATE: 2000-08-16 PRIOR FILING DATE: 2000-08-11 PRIOR FILING DATE: 2000-08-11 PRIOR FILING DATE: 1099-05-07 PRIOR FILING DATE: 1099-05-07 PRIOR APPLICATION NUMBER: US 09/275,267	PRIOR FILING DATE: 1999-03-23 PRIOR APPLICATION NUMBER: US 60/119,917 PRIOR FILING DATE: 1999-02-12 NUMBER OF SEQ ID NOS: 1304 SOFTWARE: Patent.pm SEQ ID NO 651 FIRNCH: 20674 TYPE: DNA	PRATURE: Homo sapiens FRATURE: NAME/KEY: misc feature LOCATION: 11233123 OTHER INFORMATION: 5'regulatory region FEATURE: exon NAME/KEY: exon OTHER FIROPMATION: 27	FEATURE: FEATURE: exon LOAME/KEY: exon LOAME/KEY: exon OTHER INFORMATION: exon FEATURE: NAME/KEY: exon LOAME/KEY: exon LOAME/KEY: exon OTHER INFORMATION: 5552.5633	FEATURE: NAME/KEY: exon LOCATION: 5758.5880 OTHER INFORMATION: exon 4 FEATURE: NAME/KEY: exon LOCATION: 59966099 OTHER INFORMATION: exon 5 FEATURE:	NAME/KEY: 6509 LOCATION: 63496509 CTHER INFORMATION: exon 6 FRATURE: NAME/KEY: exon LOCATION: 73797522 CTHER INFORMATION: exon 7 FRATURE: NAME/KEY: exon

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<pre>10-513-365 : polymorphic base A or G 12-206-81 : polymorphic base A or G 10-343-238 : polymorphic base C or 10-343-239 : polymorphic base A or G 10-346-233 : polymorphic base A or G 10-346-263 : polymorphic base A or G 10-346-305 : polymorphic base A or G 10-346-305 : polymorphic base A or G 10-347-141 : polymorphic base A or G 10-347-165 : polymorphic base C or 10-347-165 : polymorphic base C or 10-347-203 : polymorphic base C or 10-347-203 : polymorphic base A or G</pre>	allele 2934 ORMATION:	10-513-352	: polymorphic base A or G
allele RMATION: 10-343-231 : deletion of C ANATION: 10-343-231 : deletion of C ANATION: 12-206-366 : polymorphic base C or allele RMATION: 10-343-278 : polymorphic base C or A109 RMATION: 10-345-23 : polymorphic base A or G S003 RMATION: 10-346-263 : polymorphic base A or G allele S019 RMATION: 10-346-263 : polymorphic base A or G allele S038 RMATION: 10-346-263 : polymorphic base A or G allele S110 S110 S110 S110 S110 S110 S110 S11		-513-3	: polymorphic base A or polymorphic base A or G
allele RMATION: 12-206-366 : polymorphic base C or allele RMATION: 12-206-366 : polymorphic base C or allele RMATION: 10-343-278 : polymorphic base G or allele RVATION: 10-346-23 : polymorphic base A or G stal RVATION: 10-346-141 : polymorphic base A or G allele 613 RMATION: 10-346-263 : polymorphic base A or allele 613 RMATION: 10-346-305 : polymorphic base G or allele 643 RMATION: 10-347-74 : polymorphic base A or G allele 633 RMATION: 10-347-74 : polymorphic base A or G allele 633 RMATION: 10-347-71 : polymorphic base C or allele 633 RMATION: 10-347-165 : polymorphic base C or allele 633 RMATION: 10-347-165 : polymorphic base A or allele 633 RMATION: 10-347-203 : polymorphic base A or allele 8467 RMATION: 10-347-203 : polymorphic base A or allele 8467 RMATION: 10-347-203 : polymorphic base A or allele	RE: KEY: allele ION: 4062 INFORMATION:	-343-2	deletion of
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allele AlTO RMATION: 10-343-339 : polymorphic base G or allele RMATION: 10-346-141 : polymorphic base A or G RMATION: 10-346-141 : polymorphic base A or allele 6019 RVATION: 10-346-263 : polymorphic base G or allele 6318 RMATION: 10-346-263 : polymorphic base G or allele 6338 RMATION: 10-347-74 : polymorphic base A or G allele 6338 RMATION: 10-347-111 : polymorphic base A or allele 6336 RMATION: 10-347-165 : polymorphic base C or allele 6375 RMATION: 10-347-165 : polymorphic base C or allele 6375 RMATION: 10-347-203 : polymorphic base A or allele 8467 RMATION: 10-347-203 : polymorphic base A or allele 8467 RMATION: 10-347-203 : polymorphic base A or allele		-343-2	polymorphic base C or
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allele 6019 RMATION: 10-346-141 : polymorphic base A or allele 6141 RMATION: 10-346-263 : polymorphic base G or sallele SRMATION: 10-347-74 : polymorphic base A or G allele 633 RMATION: 10-347-711 : polymorphic base A or allele 6375 RMATION: 10-347-111 : polymorphic base G or allele 6429 SRMATION: 10-347-165 : polymorphic base C or allele 6420 SRMATION: 10-347-203 : polymorphic base A or allele 6467 SRMATION: 10-347-203 : polymorphic base A or allele		6-2	polymorphic base A or
allele 6141 RMATION: 10-346-263 : polymorphic base G or 6183 allele 6183 RMATION: 10-346-305 : polymorphic base C or allele 6318 RMATION: 10-347-74 : polymorphic base A or G allele 6375 allele 6429 SMATION: 10-347-111 : polymorphic base G or allele 6429 SMATION: 10-347-165 : polymorphic base C or allele 6457 SMATION: 10-347-203 : polymorphic base A or allele 6467 SMATION: 10-347-203 : polymorphic base A or allele	allele 6019 RMATION:	-14	polymorphic base A or
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: allele : 6429 FCXMATION: 10-347-165 : polymorphic base C or : allele : 6467 : 6467 : allele : allele : allele	: Y: allele N: 6375 NFORMATION:	-347-11	polymorphic base G or
: allele 1: 6467 JFORNATION: 10-347-203 : polymorphic base A or JFORNATION: 10-347-203 : polymorphic base A or 1: 6484	: allele 1: 6429 1FORMATION:	47	: polymorphic base C or
KBY: allele ION: 6484 THDORANTON: 10_207_020 . molumovahir hasa 2 or	r: allele 1: 6467 1FORMATION:		: polymorphic base A or
TO U SOME ATTRATOUGTON . AZZ-/ LC_AT INOTTHINGANT	Y: allele N: 6484 NFORMATION:	10-347-220	: polymorphic base A or G
əry Match 13.0%; Score 59.4; DB 4; Length 20674; st Local Similarity 49.5%; Pred: No. 0.00062; cches 153; Conservative 0; Mismatches 156; Indels 0; Gaps 0;	Query Match Best Local Similarity Matches 153; Conser	5%;	core 59.4; DB 4; Length 20674; red. No. 0.00062; Mismatches 156; Indels 0; Gaps

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